

*Don Nikodem*

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111

1633

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/388,221A DATE: 05/25/2000  
TIME: 15:49:41

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3 <110> APPLICANT: Reed, John C.  
 5 <120> TITLE OF INVENTION: Novel Card Proteins Involved in Cell Death Regulation  
 7 <130> FILE REFERENCE: P-LJ 3650  
 9 <140> CURRENT APPLICATION NUMBER: 09/388,221A  
 10 <141> CURRENT FILING DATE: 1999-09-01  
 12 <160> NUMBER OF SEQ ID NOS: 18  
 14 <170> SOFTWARE: PatentIn Ver. 2.1  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 4422  
 18 <212> TYPE: DNA  
 19 <213> ORGANISM: Homo sapiens  
 21 <220> FEATURE:  
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 23 <222> LOCATION: (1)..(4422)  
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28	1								10						15		
30	aag	aag	gag	gag	ctg	aag	gag	ttc	cag	ctt	ctg	ctc	gcc	aat	aaa	gcg	96
31	Lys	Lys	Glu	Glu	Leu	Lys	Glu	Phe	Gln	Leu	Leu	Leu	Ala	Asn	Lys	Ala	
32									25						30		
34	cac	tcc	agg	agc	tct	tcg	ggt	gag	aca	ccc	gct	cag	cca	gag	aag	acg	144
35	His	Ser	Arg	Ser	Ser	Gly	Glu	Thr	Pro	Ala	Gln	Pro	Glu	Lys	Thr		
36									35						45		
38	agt	ggc	atg	gag	gtg	gcc	tgc	tac	ctg	gtg	gtc	cag	tat	ggg	gag	cag	192
39	Ser	Gly	Met	Glu	Val	Ala	Ser	Tyr	Leu	Val	Ala	Gln	Tyr	Gly	Glu	Gln	
40									50						60		
42	cgg	gcc	tgg	gac	cta	gcc	ctc	cat	acc	tgg	gag	cag	atg	ggg	ctg	agg	240
43	Arg	Ala	Trp	Asp	Leu	Ala	Leu	His	Thr	Trp	Glu	Gln	Met	Gly	Leu	Arg	
44									65						80		
46	tca	ctg	tgc	gcc	caa	gcc	cag	gaa	ggg	gca	ggc	cac	tct	ccc	tca	tcc	288
47	Ser	Leu	Cys	Ala	Gln	Ala	Gln	Glu	Gly	Ala	Gly	His	Ser	Pro	Ser	Phe	
48									85						95		
50	ccc	tac	agc	cca	agt	gaa	ccc	cac	ctg	ggg	tct	ccc	agc	caa	ccc	acc	336
51	Pro	Tyr	Ser	Pro	Ser	Glu	Pro	His	Leu	Gly	Ser	Pro	Ser	Gln	Pro	Thr	
52									100						110		
54	tcc	acc	gca	gtg	cta	atg	ccc	tgg	atc	cat	gaa	ttg	ccg	gcg	ggg	tgc	384
55	Ser	Thr	Ala	Val	Leu	Met	Pro	Trp	Ile	His	Glu	Leu	Pro	Ala	Gly	Cys	
56									115						125		
58	acc	cag	ggc	tca	gag	aga	agg	gtt	ttg	aga	cag	ctg	cct	gac	aca	tct	432
59	Thr	Gln	Gly	Ser	Glu	Arg	Arg	Val	Leu	Arg	Gln	Leu	Pro	Asp	Thr	Ser	
60									130						140		
62	gga	cgc	cgc	tgg	aga	gaa	atc	tct	gcc	tca	ctc	tac	caa	gct	ctt		480
63	Gly	Arg	Arg	Trp	Arg	Glu	Ile	Ser	Ala	Ser	Leu	Leu	Tyr	Gln	Ala	Leu	
64									145						160		
66	cca	agc	tcc	cca	gac	cat	gag	tct	cca	agc	cag	gag	tca	ccc	aac	gcc	528
67	Pro	Ser	Ser	Pro	Asp	His	Glu	Ser	Pro	Ser	Gln	Glu	Ser	Pro	Asn	Ala	

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70	ccc aca tcc aca gca gtg ctg ggg agc tgg gga tcc cca cct cag ccc			576
71	Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro			
72	180	185	190	
74	agc cta gca ccc aga gag cag gag gct cct ggg acc caa tgg cct ctg			624
75	Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu			
76	195	200	205	
78	gat gaa acg tca gga att tac tac aca gaa atc aga gaa aga gag aga			672
79	Asp Glu Thr Ser Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg			
80	210	215	220	
82	gag aaa tca gag aaa ggc agg ccc cca tgg gca gcg gtg gta gga acg			720
83	Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr			
84	225	230	235	240
86	ccc cca cag gcg cac acc agc cta cag ccc cac cac cca tgg gag			768
87	Pro Pro Gln Ala His Thr Ser Leu Gln Pro His His Pro Trp Glu			
88	245	250	255	
90	cct tct gtg aga gag agc ctc tgt tcc aca tgg ccc tgg aaa aat gag			816
91	Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu			
92	260	265	270	
94	gat ttt aac caa aaa ttc aca cag ctg cta ctt cta caa aga cct cac			864
95	Asp Phe Asn Gln Lys Phe Thr Gln Leu Leu Leu Gln Arg Pro His			
96	275	280	285	
98	ccc aga agc caa gat ccc ctg gtc aag aga agc tgg cct gat tat gtg			912
99	Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val			
100	290	295	300	
102	gag gag aat cga gga cat tta att gag atc aga gac tta ttt ggc cca			960
103	Glu Glu Asn Arg Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro			
104	305	310	315	320
106	ggc ctg gat acc caa gaa cct cgc ata gtc ata ctg cag ggg gct gct			1008
107	Gly Leu Asp Thr Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala			
108	325	330	335	
110	gga att ggg aag tca aca ctg gcc agg cag gtg aag gaa gcc tgg ggg			1056
111	Gly Ile Gly Lys Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly			
112	340	345	350	
114	aga ggc cag ctg tat ggg gac cgc ttc cag cat gtc ttc tac ttc agc			1104
115	Arg Gly Gln Leu Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Ser			
116	355	360	365	
118	tgc aga gag ctg gcc cag tcc aag gtt gtt agt ctc gct gag ctc atc			1152
119	Cys Arg Glu Leu Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile			
120	370	375	380	
122	gga aaa gat ggg aca gcc act ccg gct ccc att aga cag atc ctg tct			1200
123	Gly Lys Asp Gly Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser			
124	385	390	395	400
126	agg cca gag cgg ctg ctc ttc atc ctc gat ggt gta gat gag cca gga			1248
127	Arg Pro Glu Arg Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly			
128	405	410	415	
130	tgg gtc ttg cag gag ccg agt tct gag ctc tgt ctg cac tgg agc cag			1296
131	Trp Val Leu Gln Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln			
132	420	425	430	

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134 cca cag ccg gcg gat gca ctg ctg ggc agt ttg ctg ggg aaa act ata	1344
135 Pro Gln Pro Ala Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile	
136 435 440 445	
138 ctt ccc gag gca tcc ttc ctg atc acg gct cgg acc aca gct ctg cag	1392
139 Leu Pro Glu Ala Ser Phe Leu Ile Thr Ala Arg Thr Thr Ala Leu Gln	
140 450 455 460	
142 aac ctc att cct tct ttg gag cag gca cgt tgg gta gag gtc ctg ggg	1440
143 Asn Leu Ile Pro Ser Leu Glu Gln Ala Arg Trp Val Glu Val Leu Gly	
144 465 470 475 480	
146 ttc tct gag tcc agc agg aag gaa tat ttc tac aga tat ttc aca gat	1488
147 Phe Ser Glu Ser Ser Arg Lys Glu Tyr Phe Tyr Arg Tyr Phe Thr Asp	
148 485 490 495	
150 gaa agg caa gca att agg gcc ttt agg ttg gtc aaa tca aac aaa gag	1536
151 Glu Arg Gln Ala Ile Arg Ala Phe Arg Leu Val Lys Ser Asn Lys Glu	
152 500 505 510	
154 ctc tgg gcc ctg tgt ctt gtg ccc tgg gtg tcc tgg ctg gcc tgc act	1584
155 Leu Trp Ala Leu Cys Leu Val Pro Trp Val Ser Trp Leu Ala Cys Thr	
156 515 520 525	
158 tgc ctg atg cag cag atg aag cgg aag gaa aaa ctc aca ctg act tcc	1632
159 Cys Leu Met Gln Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser	
160 530 535 540	
162 aag acc acc aca acc ctc tgt cta cat tac ctt gcc cag gct ctc caa	1680
163 Lys Thr Thr Thr Leu Cys Leu His Tyr Leu Ala Gln Ala Leu Gln	
164 545 550 555 560	
166 gct cag cca ttg gga ccc cag ctc aga gac ctc tgc tct ctg gct gct	1728
167 Ala Gln Pro Leu Gly Pro Gln Leu Arg Asp Leu Cys Ser Leu Ala Ala	
168 565 570 575	
170 gag ggc atc tgg caa aaa aag acc ctt ttc agt cca gat gac ctc agg	1776
171 Glu Gly Ile Trp Gln Lys Lys Thr Leu Phe Ser Pro Asp Asp Leu Arg	
172 580 585 590 590	
174 aag cat ggg tta gat ggg gcc atc atc tcc acc ttc ttg aag atg ggt	1824
175 Lys His Gly Leu Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly	
176 595 600 605	
178 att ctt caa gag cac ccc atc cct ctg agc tac agc ttc att cac ctc	1872
179 Ile Leu Gln Glu His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu	
180 610 615 620	
182 tgt ttc caa gag ttc ttt gca gca atg tcc tat gtc ttg gag gat gag	1920
183 Cys Phe Gln Glu Phe Phe Ala Ala Met Ser Tyr Val Leu Glu Asp Glu	
184 625 630 635 640	
186 aag ggg aga ggt aaa cat tct aat tgc atc ata gat ttg gaa aag acg	1968
187 Lys Gly Arg Gly Lys His Ser Asn Cys Ile Ile Asp Leu Glu Lys Thr	
188 645 650 655	
190 cta gaa gca tat gga ata cat ggc ctg ttt ggg gca tca acc aca cgt	2016
191 Leu Glu Ala Tyr Gly Ile His Gly Leu Phe Gly Ala Ser Thr Thr Arg	
192 660 665 670	
194 ttc cta ttg ggc ctg tta agt gat gag ggg gag aga gag atg gag aac	2064
195 Phe Leu Leu Gly Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn	
196 675 680 685	
198 atc ttt cac tgc cgg ctg tct cag ggg agg aac ctg atg cag tgg gtc	2112

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203	Pro	Ser	Leu	Gln	Leu	Leu	Gln	Pro	His	Ser	Leu	Glu	Ser	Leu	His		
204	705				710				715							720	
206	tgc	ttt	tac	gag	act	cgg	aac	aaa	acg	ttc	ctg	aca	caa	gtg	atg	gcc	2208
207	Cys	Leu	Tyr	Glu	Thr	Arg	Asn	Lys	Thr	Phe	Leu	Thr	Gln	Val	Met	Ala	
208										725		730				735	
210	cat	ttc	gaa	gaa	atg	ggc	atg	tgt	gta	gaa	aca	gac	atg	gag	ctc	tta	2256
211	His	Phe	Glu	Glu	Met	Gly	Met	Cys	Val	Glu	Thr	Asp	Met	Glu	Leu	Leu	
212					740				745							750	
214	gtg	tgc	act	ttc	tgc	att	aaa	ttc	agc	cgc	cac	gtg	aag	aag	ctt	cag	2304
215	Val	Cys	Thr	Phe	Cys	Ile	Lys	Phe	Ser	Arg	His	Val	Lys	Lys	Leu	Gln	
216						755			760			765					
218	ctg	att	gag	ggc	agg	cag	cac	aga	tca	aca	tgg	agc	ccc	acc	atg	gta	2352
219	Leu	Ile	Glu	Gly	Arg	Gln	His	Arg	Ser	Thr	Trp	Ser	Pro	Thr	Met	Val	
220						770			775			780					
222	gtc	ctg	ttc	agg	tgg	gtc	cca	gtc	aca	gat	gcc	tat	tgg	cag	att	ctc	2400
223	Val	Leu	Phe	Arg	Trp	Val	Pro	Val	Thr	Asp	Ala	Tyr	Trp	Gln	Ile	Leu	
224						785			790			795				800	
226	ttc	tcc	gtc	ctc	aag	gtc	acc	aga	aac	ctg	aag	gag	ctg	gac	cta	agt	2448
227	Phe	Ser	Val	Leu	Lys	Val	Thr	Arg	Asn	Leu	Lys	Glu	Leu	Asp	Leu	Ser	
228						805			810			815					
230	gga	aac	tcg	ctg	agc	cac	tct	gca	gtg	aag	agt	ctt	tgt	aag	acc	ctg	2496
231	Gly	Asn	Ser	Leu	Ser	His	Ser	Ala	Val	Lys	Ser	Leu	Cys	Lys	Thr	Leu	
232						820			825			830					
234	aga	cgc	cct	cgc	tgc	ctc	ctg	gag	acc	ctg	cgg	tgg	gct	ggc	tgt	ggc	2544
235	Arg	Arg	Pro	Arg	Cys	Leu	Leu	Glu	Thr	Leu	Arg	Leu	Ala	Gly	Cys	Gly	
236						835			840			845					
238	ctc	aca	gct	gag	gac	tgc	aag	gac	ctt	gcc	ttt	ggg	ctg	aga	gcc	aac	2592
239	Leu	Thr	Ala	Glu	Asp	Cys	Lys	Asp	Leu	Ala	Phe	Gly	Leu	Arg	Ala	Asn	
240						850			855			860					
242	cag	acc	ctg	acc	gag	ctg	gac	ctg	agc	ttc	aat	gtg	ctc	acg	gat	gct	2640
243	Gln	Thr	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Phe	Asn	Val	Leu	Thr	Asp	Ala	
244						865			870			875				880	
246	gga	gcc	aaa	cac	ctt	tgc	cag	aga	ctg	aga	cag	ccg	agc	tgc	aag	cta	2688
247	Gly	Ala	Lys	His	Leu	Cys	Gln	Arg	Leu	Arg	Gln	Pro	Ser	Cys	Lys	Leu	
248						885			890			895					
250	cag	cga	ctg	cag	ctg	gtc	agc	tgt	ggc	ctc	acg	tct	gac	tgc	tgc	cag	2736
251	Gln	Arg	Leu	Gln	Leu	Val	Ser	Cys	Gly	Leu	Thr	Ser	Asp	Cys	Cys	Gln	
252						900			905			910					
254	gac	ctg	gcc	tct	gtg	ctt	agt	gcc	agc	ccc	agc	ctg	aag	gag	cta	gac	2784
255	Asp	Leu	Ala	Ser	Val	Leu	Ser	Ala	Ser	Pro	Ser	Leu	Lys	Glu	Leu	Asp	
256						915			920			925					
258	ctg	cag	cag	aac	aac	ctg	gat	gac	gtt	ggc	gtg	cga	ctg	ctc	tgt	gag	2832
259	Leu	Gln	Gln	Asn	Asn	Leu	Asp	Asp	Val	Gly	Val	Arg	Leu	Cys	Glu		
260						930			935			940					
262	ggg	ctc	agg	cat	cct	gcc	tgc	aaa	ctc	ata	cgc	ctg	ggg	ctg	gac	cag	2880
263	Gly	Ile	Leu	Arg	His	Pro	Ala	Cys	Lys	Leu	Ile	Arg	Leu	Gly	Leu	Asp	Gln

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267	Thr Thr Leu Ser Asp Glu Met Arg Gln Glu Leu Arg Ala Leu Glu Gln				
268	965	970	975		
270	gag aaa cct cag ctg ctc atc ttc agc aga cgg aaa cca agt gtg atg				2976
271	Glu Lys Pro Gln Leu Leu Ile Phe Ser Arg Arg Lys Pro Ser Val Met				
272	980	985	990		
274	acc cct act gag ggc ctg gat acg gga gag atg agt aat agc aca tcc				3024
275	Thr Pro Thr Glu Gly Leu Asp Thr Gly Glu Met Ser Asn Ser Thr Ser				
276	995	1000	1005		
278	tca ctc aag cgg cag aga ctc gga tca gag agg gcg gct tcc cat gtt				3072
279	Ser Leu Lys Arg Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser His Val				
280	1010	1015	1020		
282	gct cag gct aat ctc aaa ctc ctg gac gtg agc aag atc ttc cca att				3120
283	Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe Pro Ile				
284	1025	1030	1035	1040	
286	gct gag att gca gag gaa agc tcc cca gag gta ccc gtg gaa ctc				3168
287	Ala Glu Ile Ala Glu Ser Ser Pro Glu Val Val Pro Val Glu Leu				
288	1045	1050	1055		
290	ttg tgc gtg cct tct gcc tct caa ggg gac ctg cat acg aag cct				3216
291	Leu Cys Val Pro Ser Pro Ala Ser Gln Gly Asp Leu His Thr Lys Pro				
292	1060	1065	1070		
294	ttg ggg act gac gat gac ttc tgg ggc ccc acg ggg cct gtg gct act				3264
295	Leu Gly Thr Asp Asp Asp Phe Trp Gly Pro Thr Gly Pro Val Ala Thr				
296	1075	1080	1085		
298	gag gta gtt gac aaa gaa aag aac ttg tac cga gtt cac ttc cct gta				3312
299	Glu Val Val Asp Lys Glu Lys Asn Leu Tyr Arg Val His Phe Pro Val				
300	1090	1095	1100		
302	gct ggc tcc tac cgc tgg ccc aac acg ggt ctc tgc ttt gtg atg aga				3360
303	Ala Gly Ser Tyr Arg Trp Pro Asn Thr Gly Leu Cys Phe Val Met Arg				
304	1105	1110	1115	1120	
306	gaa gcg gtg acc gtt gag att gaa ttc tgt gtg tgg gac cag ttc ctg				3408
307	Glu Ala Val Thr Val Glu Ile Glu Phe Cys Val Trp Asp Gln Phe Leu				
308	1125	1130	1135		
310	ggt gag atc aac cca cag cac agc tgg atg gtg gca ggg cct ctg ctg				3456
311	Gly Glu Ile Asn Pro Gln His Ser Trp Met Val Ala Gly Pro Leu Leu				
312	1140	1145	1150		
314	gac atc aag gct gag cct gga gct gtg gaa gct gtg cac ctc cct cac				3504
315	Asp Ile Lys Ala Glu Pro Gly Ala Val Glu Ala Val His Leu Pro His				
316	1155	1160	1165		
318	ttt gtg gct ctc caa ggg ggc cat gtg gac aca tcc ctg ttc caa atg				3552
319	Phe Val Ala Leu Gln Gly His Val Asp Thr Ser Leu Phe Gln Met				
320	1170	1175	1180		
322	gcc cac ttt aaa gag gag ggg atg ctc ctg gag aag cca gcc agg gtg				3600
323	Ala His Phe Lys Glu Glu Gly Met Leu Leu Glu Lys Pro Ala Arg Val				
324	1185	1190	1195	1200	
326	gag ctg cat cac ata gtt ctg gaa aac ccc agc ttc tcc ccc ttg gga				3648
327	Glu Leu His His Ile Val Leu Glu Asn Pro Ser Phe Ser Pro Leu Gly				
328	1205	1210	1215		

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